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RAW SEQUENCE LISTING

DATE: 10/01/2002

PATENT APPLICATION: US/10/009,445A

TIME: 11:22:36

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3 <110> APPLICANT: Barclay, Neil A.
 4 Brown, Marion H.
 5 Gorman, Daniel M.
 6 Lanier, Lewis L.
 7 Wright, Gavin J.
 8 Cherwinski, Holly
 9 Phillips, Joseph H.
 10 Hoek, Robert M.
 11 Sedgwick, Jonathon D.
 13 <120> TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
 15 <130> FILE REFERENCE: DX01052K1
 17 <140> CURRENT APPLICATION NUMBER: 10/009,445A
 C--> 18 <141> CURRENT FILING DATE: 2002-09-04
 20 <150> PRIOR APPLICATION NUMBER: PCT/US00/12998
 21 <151> PRIOR FILING DATE: 2000-05-11
 23 <150> PRIOR APPLICATION NUMBER: 9911123.9 GB
 24 <151> PRIOR FILING DATE: 1999-05-13
 26 <150> PRIOR APPLICATION NUMBER: 9925989.7 GB
 27 <151> PRIOR FILING DATE: 1999-11-03
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 51 cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt 162
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 53 10 15 20
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67	ata acc ctc aga gga cag cct tcc tgc ata ata tcc tac aaa gca gac	354
68	Ile Thr Leu Arg Gly Gln Pro Ser Cys Ile Ile Ser Tyr Lys Ala Asp	
69	75 80 85	
71	aca agg gag acc cat gaa agc aac tgc tcg gac aga agc atc acc tgg	402
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75	gcc tcc aca cct gac ctc gct cct gac ctt cag atc agt gca gtg gcc	450
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79	ctc cag cat gaa ggg cgt tac tca tgt gat ata gca gta cct gac ggg	498
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83	aat ttc caa aac atc tat gac ctc caa gtg ctg gtg ccc cct gaa gta	546
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173 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser
174 65          70          75          80
177 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn
178          85          90          95
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182          100          105          110
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186          115          120          125
189 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu
190          130          135          140
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194 145          150          155          160
197 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser
198          165          170          175
201 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn
202          180          185          190
205 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val
206          195          200          205
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213 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
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257 aagttgacca gagaggggtct caccatgcmc acagttcctt ctgtaccagt gtggaggaaa      180
259 agtactgagt gaagggcaga aaaagagaaa acagaaa atg ctc tgc cct tgg aga      234
260                                     Met Leu Cys Pro Trp Arg
261                                     1          5
263 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc      282
264 Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
265          10          15          20
267 gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act      330
268 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
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271 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa      378
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273          40          45          50
275 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act      426
276 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
277 55          60          65          70
279 tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct      474
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281          75          80          85
283 atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga      522
284 Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg
285          90          95          100
287 ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc      570
288 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
289          105          110          115
291 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct      618
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293          120          125          130
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300 Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg
301                      155                      160                      165
303 gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa      762
304 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
305                      170                      175                      180
307 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct      810
308 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
309                      185                      190                      195
311 gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa      858
312 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
313      200                      205                      210
315 tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag      906
316 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
317 215                      220                      225                      230
319 gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc      954
320 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
321                      235                      240                      245
323 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa      1002
324 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
325                      250                      255                      260
327 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta      1050
328 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Tyr Leu
329      265                      270                      275
331 gac cat cgt ggg att cat ttg gtt gtt gaa agt caa tgg ctg cag aaa      1098
332 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
333      280                      285                      290
335 ata taaattgaat aaaacagaat ctactccagt tggtgaggag gatgaaatgc      1151
336 Ile
337 295
339 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaagggtga      1211
341 aggcattctga ggcattacaa agtgaagttg acacagacct ccatacttta taagttggtg      1271
343 gactctagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct      1331
345 tacagttcta gaatgaagac ttatattgaa attaggtttt ccaagggttct tagaagacat      1391
347 tttaatggat tctcattcat acccttgat atttggaatt ttgattctt agctgctacc      1451
349 agctagttct ctgaagaact gatgttatta caaagaaaat acatgccccat gaccaaatat      1511
351 tcaaattgtg caggacagta aataatgaaa accaaatttc ctcaagaaat aactgaagaa      1571
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368      20                      25                      30

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Seq#:21; N Pos. 711,714,723,726,732,735,738,747,750,762,765,768,771,774,777
Seq#:21; N Pos. 780,789,792,798,807,819,822,834,837,843,846,858,861,867,873
Seq#:21; N Pos. 879,891,900,906,909,912,915,918,939,945,948,954,969,972,981
Seq#:21; N Pos. 984,993,999,1002,1008,1011,1017,1023,1029,1035,1041,1044
Seq#:24; N Pos. 9,12,15,18,24,27,30,33,36,39,60,63,66,69,72,78,93,108,111
Seq#:24; N Pos. 114,117,120,123,129,135,138,144,147,165,168,171,183,186,189
Seq#:24; N Pos. 192,201,204,207,213,231,237,240,243,249,255,264,276,285,288
Seq#:24; N Pos. 294,297,300,309,315,318,321,324,333,336,342,351,354,357,360
Seq#:24; N Pos. 363,375,378,384,396,399,402,408,414,423,432,438,441,444,447
Seq#:24; N Pos. 450,456,459,468,471,480,483,486,489,498,504,507,513,516,519
Seq#:24; N Pos. 528,534,537,543,552,555,561,567,573,579,582,585,588,591,594
Seq#:24; N Pos. 597,600,624,627,630,633,636,642,645,648,654,657,660,669,672
Seq#:24; N Pos. 675,684,687,693,696,702,705,708,711,714,717,720,723,729,735
Seq#:24; N Pos. 744,747,750,753,762,765,771,774,780,795,804,807,810